

QY 438 LDDMIKEIDLNDGKIDFSEETAMRKGDGVRSRRTMMKNLNFNIADFGVDG---EKS 493

Qy	494	DD	495
nb	421	DD	422

RESULT 5  
AAW93256  
Protein standard: 512 AA.

XX  
AC  
AAW93256:XX  
of 1000 (first entry)[illegible]

XX  
XX  
KW  
KW  
KW  
KW

Glycine max.

XX Location/Qualifiers

FH	Key	Location/Qualifiers
FT	Region	41..46

FT	region	/note= "protein kinase sequence"
FT	region	158..163
FT	region	158..163

FI	region	/note= "protein kinase sequence
FT		198..205
FI	region	

Region	/note= "protein kinase sequence
FT	348 360
FT	348 360

FT	Binding-site	/note= "calcium binding site"
340.300		
FT		
300		
FT		

FT	Binding-site	388..399	/note= "calcium binding site"
FT			

FT	Binding-site	425..435	
FT		/note= "calcium binding site"	

FT	Binding-site	458..468	"calcium binding site"
GT		/note=	

XX  
DN  
W09902655-A1.

XX  
21--TAN-1999.

XX 02 1099. 98WO-US14109.

XX 07118-0889655

PR 06-007-1537  
XX

PA (KENT ) UNIV KENTUCKY RES ESTABL  
yy

PT Chappell J, Lusso MFG;

XX WPT: 1999-120859/10.

XX New polynucleotides based on calcium dependent protein kinase genes  
PT New polynucleotides based on calcium dependent protein kinase genes

XX  
Figure 4: Fig 4: 51pp: English.

Example 4: *Fig. 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100*

This invention describes a novel nucleic acid molecule and its encoded protein that are induced upon pathogen invasion or elicitor treatment. The products of the invention are functional in plants, plant tissue and plant cells for inducible gene expression and altering the disease resistance phenotype of plants. The products of the invention are related to calcium dependent protein kinase (CDPK) genes. The invention describes the isolation of a novel tobacco CDPK protein fragment and its encoding nucleic acid, isolated from a cell suspension culture derived from a tobacco cultivar KV14 explant, after growth in the presence of the elicitor parasiticein. This sequence represents the soybean CDPK protein.

XX	Sequence	512 AA;
50		

XX 50

10-SEP-1999; 99US-0153070.  
13-SEP-1999; 99US-0153758.  
15-SEP-1999; 99US-0154018.  
16-SEP-1999; 99US-0154039.  
20-SEP-1999; 99US-0154779.  
22-SEP-1999; 99US-0155139.  
23-SEP-1999; 99US-0155486.  
24-SEP-1999; 99US-0156559.  
28-SEP-1999; 99US-0156458.  
29-SEP-1999; 99US-0156596.  
04-OCT-1999; 99US-0157117.  
05-OCT-1999; 99US-0157753.  
06-OCT-1999; 99US-0157865.  
07-OCT-1999; 99US-0158029.  
08-OCT-1999; 99US-0158232.  
12-OCT-1999; 99US-0158369.  
13-OCT-1999; 99US-0159293.  
13-OCT-1999; 99US-0159294.  
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14-OCT-1999; 99US-0159329.  
14-OCT-1999; 99US-0159330.  
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14-OCT-1999; 99US-0159637.  
14-OCT-1999; 99US-0159638.  
18-OCT-1999; 99US-0159584.  
21-OCT-1999; 99US-0160741.  
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21-OCT-1999; 99US-0160768.  
21-OCT-1999; 99US-0160770.  
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21-OCT-1999; 99US-0160814.  
21-OCT-1999; 99US-0160815.  
21-OCT-1999; 99US-0160815.  
22-OCT-1999; 99US-0160880.  
22-OCT-1999; 99US-0160981.  
22-OCT-1999; 99US-0160989.  
25-OCT-1999; 99US-0161404.  
25-OCT-1999; 99US-0161405.  
25-OCT-1999; 99US-0161406.  
25-OCT-1999; 99US-0161406.  
26-OCT-1999; 99US-0161359.  
26-OCT-1999; 99US-0161360.  
26-OCT-1999; 99US-0161361.  
28-OCT-1999; 99US-0161920.  
28-OCT-1999; 99US-0161992.  
28-OCT-1999; 99US-0161993.  
28-OCT-1999; 99US-0162142.  
28-OCT-1999; 99US-0162142.

Query Match	79.68;	Score 2064;	DB 21;	Length 425;
Beet Local Similarity	94.5%;	Pred. No. 2.7e-175;		
Matches 399;	Conservative 6;	Mismatches 13;	Indels 4;	Gaps 1;
Qy	78	MHLLSEHPNVVRIKGTVEDSVFVHIVMECEGGELFDRIVSKGHFSEREAVKLIKTILGV	137	
Db	1	MHLLSEHPNVVRIKGTIVEDSVFVHIVMECEGGELFDRIVSKGCFSEAAKLIKTILGV	60	
Qy	138	VEACHSLGVMRDLKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLDYVVGGSPYYVAPE	197	
Db	61	VEACHSLGVMRDLKPENFLFDSPPSDDAKLKATDFGLSVFYKPGQYLDYVVGGSPYYVAPE	120	
Qy	198	VLKCKVGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKLPKSPMPWTISEAA	257	
Db	121	VLKCKVGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKIDFKSPMPWTISEGA	180	
Qy	258	KOLLYKMLRSPKGRISAHEALCHPWIVDEQAAPKPLDPAVLSRLKQFSQNNKIKKQAL	317	
Db	181	KOLLYKMLDRSPKKRISAHEALCHPWIVDEHAAPKPLDPAVLSRLKQFSQNNKIKKQAL	240	
Qy	318	RVIAERLSBEIIGGLKELFKQIDTDNSGTTTFEELKAGLKRVCSELMSESEIKSLMDAADI	377	
Db	241	RVIAERLSBEIIGGLKELFKQIDTDNSGTTTFEELKAGLKRVCSELMSESEIKSLMDAADI	300	
Qy	378	DNSGTIDYGEFLAATLHNNKWEREEILVAAFSDFDKDGSGYTTIDELQACTFEFGLCDTP	437	
Db	301	DNSGTIDYGEFLAATLHNNKWEREENLVAFSFDKDGSGYTTIDELQACTFEFGLCDTP	360	